Amendments to the Specification

Please replace the paragraph on page 1, lines 16-22 with the following amended paragraph:

Lipases are enzymes which are involved in the breakdown of fats. Lipases are commercially important enzymes which have many current uses, including as reagents in food preparation processes (e.g., as additives to animal feeds), industrial degradative processes, crop engineering and even as treatments for several human diseases (e.g., indigestion and heartburn (e.g., for pancreatic insufficiency), secondary cystic fibrosis, Celiac disease, Crohn's disease, obesity, etc.). The activities and sequences of several hundred lipases are known. *See,* e.g., ~~www.led.uni-stuttgart.de/~~ the world wide web at led.uni-stuttgart.de/.

Please replace the paragraph on page 27, lines 25-31 with the following amended paragraph:

In addition, essentially any nucleic acid can be custom ordered from any of a variety of commercial sources, such as The Midland Certified Reagent Company (mcrc@oligos.com), The great American Gene Company (~~www.genco.com~~ the world wide web at genco.com), ExpressGen Inc. (~~www.expressgen.com~~ the world wide web at expressgen.com), Operon Technologies Inc. (Alameda, CA) and many others. Similarly, peptides and antibodies can be custom ordered from any of a variety of sources, such as PeptidoGenic (pkim@ccnet.com), HTI Bio-products, ~~inc.~~ Inc. (~~www.htibio.com~~ the world wide web at htibio.com), BMA Biomedicals Ltd. (U.K.), Bio.Synthesis, Inc., and many others.

Please replace the paragraph from page 56, line 28 to page 57, line 23 with the following amended paragraph:

Other preferred examples of algorithm that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., (1977) Nuc Acids Res 25:3389-3402 and Altschul et al., (1990) J Mol Biol 215:403-410, respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (~~www.ncbi.nlm.nih.gov/~~ the world wide web at ncbi.nlm.nih.gov/). This algorithm

involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction is halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see*, Henikoff & Henikoff, (1989) Proc Natl Acad Sci USA 89:10915) uses alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace the paragraph from page 99, line 29 to page 100, line 16 with the following amended paragraph:

In yet another aspect, in an in vivo or in vivo treatment method in which a polynucleotide construct (or composition comprising a polynucleotide construct) is used to deliver a physiologically active polypeptide to a subject, the expression of the polynucleotide construct can be induced by using an inducible on- and off-gene expression system. Examples of such on- and off-gene expression systems include the ~~Tet-On™~~ TET-ON™ Gene Expression System and ~~Tet-Off™~~ TET-OFF™ Gene Expression System (*see*, e.g., Clontech Catalog 2000, pg. 110-111 for a detailed description of each such system), respectively. Other controllable or inducible on- and off-gene expression systems are known to those of ordinary skill in the art. With such system, expression of

the target nucleic acid of the polynucleotide construct can be regulated in a precise, reversible, and quantitative manner. Gene expression of the target nucleic acid can be induced, for example, after the stable transfected cells containing the polynucleotide construct comprising the target nucleic acid are delivered or transferred to or made to contact the tissue site, organ or system of interest. Such systems are of particular benefit in treatment methods and formats in which it is advantageous to delay or precisely control expression of the target nucleic acid (e.g., to allow time for completion of surgery and/or healing following surgery; to allow time for the polynucleotide construct comprising the target nucleic acid to reach the site, cells, system, or tissue to be treated; to allow time for the graft containing cells transformed with the construct to become incorporated into the tissue or organ onto or into which it has been spliced or attached, etc.).

Please replace the paragraph on page 106, lines 18-28 with the following amended paragraph:

Similarly, standard desktop applications such as word processing software (e.g., Microsoft ~~Word™~~ WORD™ or Corel ~~WordPerfect™~~ WORDPERFECT™) and database software (e.g., spreadsheet software such as Microsoft ~~Excel™~~ EXCEL™, Corel ~~Quattro Pro™~~ QUATTRO PRO™, or database programs such as Microsoft ~~Access™~~ ACCESS™ or ~~Paradox™~~ PARADOX™) can be adapted to the present invention by inputting a character string corresponding to the lipase homologues of the invention (either nucleic acids or proteins, or both). For example, the integrated systems can include the foregoing software having the appropriate character string information, e.g., used in conjunction with a user interface (e.g., a GUI in a standard operating system such as a Windows, Macintosh or LINUX system) to manipulate strings of characters. As noted, specialized alignment programs such as BLAST can also be incorporated into the systems of the invention for alignment of nucleic acids or proteins (or corresponding character strings).